

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT (other than U.S.): AMRAD CORPORATION LIMITED
(U.S. only): **Douglas James HILTON**

(ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: AU PROVISIONAL
(B) FILING DATE: 05-SEP-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES DR, E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777
(B) TELEFAX: +61 3 9254 2770

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 45..1340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC	56
Met Ser Ser Ser	
1	
TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG	104
Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val	
5 10 15 20	
TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG	152
Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln	
25 30 35	
TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT	200
Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser	
40 45 50	
GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC	248
Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu	
55 60 65	

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CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val 70 75 80	296
GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val 85 90 95 100	344
TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro 105 110 115	392
GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp 120 125 130	440
AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr 135 140 145	488
AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser 150 155 160	536
ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys 165 170 175 180	584
GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr 185 190 195	632
GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu 200 205 210	680
CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser 215 220 225	728
GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala 230 235 240	776
TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr 245 250 255 260	824
CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu 265 270 275	872
GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg 280 285 290	920

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GTC AG¹ GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC 968
 Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser
 295 300 305

CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA 1016
 Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile
 310 315 320

CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT 1064
 Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala
 325 330 335 340

CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA 1112
 Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro
 345 350 355

AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG 1160
 Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala
 360 365 370

TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA 1208
 Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala
 375 380 385

CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA 1256
 Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln
 390 395 400

AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA 1304
 Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly
 405 410 415 420

ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTTCATC 1350
 Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
 425 430

TGTAACCCGG TCAGACTGGG GGCAGAAAGA GGCGGGGCAG TGGATCCCTG TGGATGGAGG 1410

TCTCAGCTGA AAGTCTGAGC TCTTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT 1470

GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA 1530

AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT 1590

GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA 1650

GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAA 1705

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala
 1           5           10           15
Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
          20           25           30
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys
          35           40           45
Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp
          50           55           60
Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val
          65           70           75           80
Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr
          85           90           95
Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
          100          105          110
Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
          115          120          125
Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
          130          135          140
Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
          145          150          155          160
Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
          165          170          175
Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
          180          185          190
Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
          195          200          205
Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
          210          215          220

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Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp
 225 230 235 240
 Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe
 245 250 255
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
 260 265 270
 Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
 275 280 285
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
 290 295 300
 Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu
 305 310 315 320
 Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu
 325 330 335
 Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu
 340 345 350
 Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val
 355 360 365
 Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val
 370 375 380
 Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys
 385 390 395 400
 Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu
 405 410 415
 Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
 420 425 430

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1800 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 128..1396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTCTCC TAGGAAGCCT CAGTTTGGGA 60
 GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTGGAC TCTACCTCTC 120
 CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC 169
 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala
 1 5 10
 GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG 217
 Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp
 15 20 25 30
 GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG 265
 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu
 35 40 45
 TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT 313
 Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp
 50 55 60
 GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA 361
 Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu
 65 70 75
 CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC 409
 Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys
 80 85 90
 CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC 457
 Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly
 95 100 105 110

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TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu 115 120 125	505
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr 130 135 140	553
CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT GAT AGC Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser 145 150 155	601
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro 160 165 170	649
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln 175 180 185 190	697
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr 195 200 205	745
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro 210 215 220	793
CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg 225 230 235	841
GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu 240 245 250	889
CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser 255 260 265 270	937
ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala 275 280 285	985
GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala 290 295 300	1033
GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr 305 310 315	1081
GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln 320 325 330	1129

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CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC      1177
Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser
335                      340                      345                      350

CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG      1225
Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln
355                      360                      365

GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG CGA CTG GTG      1273
Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val
370                      375                      380

GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG      1321
Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly
385                      390                      395

AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG      1369
Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val
400                      405                      410

GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT      1416
Asp Arg Arg Pro Gly Ala Pro Asn Leu
415                      420

CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA      1476

GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGA GCCCATTTCT GTGAGACCCT      1536

GTATTTCAAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTCACCCCA GAGTTGGAGT      1596

TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG      1656

AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG      1716

TCCTTGCTC TTGGCCTTTC CCCTGTCAGG GGTGTGTCAG GTGTGAATAA AGAGAATAAG      1776

GAAGTTCTTG GAGATTATAC TCAG      1800

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
 1              5              10              15

Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
20              25              30

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Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys
 35 40 45
 Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu
 50 55 60
 Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val
 65 70 75 80
 Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr
 85 90 95
 Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro
 100 105 110
 Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
 115 120 125
 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
 130 135 140
 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
 145 150 155 160
 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
 165 170 175
 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
 180 185 190
 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr Arg Leu
 195 200 205
 Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly
 210 215 220
 Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg Ala Ser
 225 230 235 240
 Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys
 245 250 255
 Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val
 260 265 270
 Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu
 275 280 285
 Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr
 290 295 300
 Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr
 305 310 315 320
 Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu
 325 330 335

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[illegible]

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

(A/G) CTCCA (C/T) T C (A/G) CTCCA

15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(A/G) CTCCA (A/G) T C (A/G) CTCCA

15

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(A/G)CTCCA(N)GC(C/T)CTCCA

15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

(A/G)CTCCA(N)GG (A/G)CTCCA

15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

(A/G)CTCCA(C/T)T T(A/G)CTCCA

15

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTCCACGG TGGAGCCCAT TGGCT

25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCACACGCGG TACGAGTCAG TGCCAGGGAC

30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAAGTTCA GCCTGGTTAA G

21

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

24

CTTATGAGTA TTTCTTCCAG GGTA

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

24

CCCTTCATTG ACCTCAACTA CATG

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

24

CATGCCAGTG AGCTTCCCGT TCAG

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTCCTCCA GGGGTCCAGT ATGG

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGGCCTCC AGAGGGT

17

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCCTGTACT TGGAGTCCAG G

21

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(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

GGAAAGCTGT GGC GTGATGG CCGTGGGGCA

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

22

GGGCGGAGGC CGCTGGCGGG CG

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

23

TTATCAGCTG AAGTTCTCTG GGG

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(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

G/ACTCCANGCG/A CTCAA

15

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCTTCTAGA TCCCCCTGCC CCCAAGCT

28

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACTTTCTAGA TTATTGCTCC AAGGGGTCCC TGTG

34